

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 08:20:15 ; Search time 76.45 Seconds

(without alignments)
176,502 Million cell updates/sec

Title: US-09-351-778a-9

Sequence: 1 MTCSTIAPTDTYRNTATAGL.....ICCLRRRARPRPIRIVL 78

Scoring table: OLIGO

Searched: 562222 segs, 172994929 residues

Word size: 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SPREMBL_19:

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	92.3	101	12	091023 human adeno
2	56	71.8	101	12	091236 human adeno
3	18	23.1	94	12	012392 human adeno
4	7	9.0	83	10	086422 spiroplasma
5	7	9.0	87	10	084862 oryza sativ
6	7	9.0	160	16	098268 rhizobium 1
7	7	9.0	160	16	092XL7 rhizobium m
8	7	9.0	197	16	09JSC7 chlamydia p
9	7	9.0	228	2	09RHX8 pseudomonas
10	7	9.0	245	8	09T3Y9 nephroselmt
11	7	9.0	316	10	09C9X6 arabidopsis
12	7	9.0	387	16	099X15 staphylococ
13	7	9.0	391	16	0876C3 clostridium
14	7	9.0	392	10	08AX94 oryza sativ
15	7	9.0	490	10	09FSS8 oryza sativ
16	7	9.0	536	5	045994 caenorhabdi

17	7	9.0	604	5	09VQ31 drosophila
18	7	9.0	635	5	09VJ77 drosophila
19	7	9.0	649	5	09NKD0 drosophila
20	7	9.0	965	2	032494 bacteroides
21	7	9.0	1175	16	091356 pseudomonas
22	7	9.0	2689	5	095Y78 leishmania
23	6	7.7	26	4	09BUB3 homo sapien
24	6	7.7	53	13	09YH36 homo sapien
25	6	7.7	64	2	09E347 streptomyces
26	6	7.7	69	13	09DEC6 gallus gall
27	6	7.7	73	15	087603 chimpanzee
28	6	7.7	76	4	09GEN4 homo sapien
29	6	7.7	77	12	064888 avian adeno
30	6	7.7	89	10	094J51 oryza sativ
31	6	7.7	89	16	09A487 canidacter
32	6	7.7	91	4	09H4V4 homo sapien
33	6	7.7	94	16	09PCB2 xyella fas
34	6	7.7	94	16	09PCAS xyella fas
35	6	7.7	95	11	09QZG8 raltus norv
36	6	7.7	97	3	09Y7L9 schizosacch
37	6	7.7	113	16	09K1B1 neisseria m
38	6	7.7	113	16	09JX91 streptomyces
39	6	7.7	115	2	09KXU2 ashya goss
40	6	7.7	115	3	09P8V1 pseudomonas
41	6	7.7	119	16	09HAX8 frankia sp.
42	6	7.7	126	2	09Z5Y0 rhizobium m
43	6	7.7	126	16	092VV9 vibrio para
44	6	7.7	128	2	P74950 sulfolobus
45	6	7.7	129	12	0914M0

ALIGNMENTS

RESULT 1
ID 091023 PRELIMINARY; PRT: 101 AA.
AC 091023:
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE 11.6K PROTEIN.
OS human adenovirus type 2.
OC viruses: dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=105;
RA Borchering F., Pring-Akerblom P.;
RT "Adenoviruses of subgenus c with different organ tropism."
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ293915; CAC67721.1;
SQ SEQUENCE 101 AA; 11662 MW; 914F50AC2F8B284F CRC64;

Query Match 92.3%; Score 72; DB 12; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.4e-70;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 APTDYYRNTATGTLTSLALNPQVHAFAVNDMAISLDMWFSIALMFVCLIIIMLIICCKRRR 66
DB 7 APTDYYRNTATGTLTSLALNPQVHAFAVNDMAISLDMWFSIALMFVCLIIIMLIICCKRRR 66
QY 67 ARPIYRPIIVL 78
DB 67 ARPIYRPIIVL 78

RESULT 2
ID 091236 PRELIMINARY; PRT: 101 AA.
AC 091236:
DT 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE 11.6K PROTEIN.
 OS Human adenovirus type 2.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 NC NCB1_TaxID=10515;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PREI:
 RA Borchering F., Pring-Akerblom P.;
 RT "Adenoviruses of subgenus C with different organ tropism."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ293913; CAC67704.1;
 SO SEQUENCE 101 AA; 11704 MW; E13857DC5891E85B CRC64;

Query Match 71.8%; Score 56; DB 12; Length 101;
 Best Local Similarity 100.0%; Pred. No. 7.2e-53;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 ALNLPQVNAFVNDASLDMMFSLAMFVCLIMLCLCKRRRRPRPIYPIVL 78
 DB 23 ALNLPQVNAFVNDASLDMMFSLAMFVCLIMLCLCKRRRRPRPIYPIVL 78

RESULT 3
 ID 012392 PRELIMINARY; PRT; 94 AA.
 AC 012392;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-JAN-1998 (Tremblrel. 05, Last annotation update)
 DE 11.6K PROTEIN.
 GN AD1/E3-11.6K.
 OS Human adenovirus type 1.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 NC NCB1_TaxID=10533;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HANNOVER / ADRIAN;
 RA Reichmann H., Scharschmidt E., Geisler B., Hausmann J., Ortman D.,
 RA Bauer U., Flunker G., Seidel W.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y11032; CAA72127.1;
 S0 SEQUENCE 94 AA; 10674 MW; D1148B5AF771862 CRC64;

Query Match 23.1%; Score 18; DB 12; Length 94;
 Best Local Similarity 100.0%; Pred. No. 9.5e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 MMFSLAMFVCLIML 58
 DB 35 MMFSLAMFVCLIML 52

RESULT 4
 ID 088422 PRELIMINARY; PRT; 83 AA.
 AC 088422;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE SPV1-C74, COMPLETE GENOME.
 OS Spiroplasma virus.
 OC Viruses; unclassified viruses.
 NC NCB1_TaxID=12338;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPV1-C74;
 RA Bedard C.M., Aulio P., Bove J., Renaudin J.;
 RT "Spiroplasma citri virus SpV1. Characterization of viral sequences

RT present in the spiroplasma host chromosome.";
 RL Curr. Microbiol. 32:1-7(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPV1-C74;
 RA Renaudin J.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U28974; AAA85015.1;
 SO SEQUENCE 83 AA; 9398 MW; DA969373B02BFFA8 CRC64;

Query Match 9.0%; Score 7; DB 12; Length 83;
 Best Local Similarity 100.0%; Pred. No. 7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 TGLTSAL 24
 DB 30 TGLTSAL 36

RESULT 5
 ID 09462 PRELIMINARY; PRT; 87 AA.
 AC 09462;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HYPOTHETICAL 9.9 KDA PROTEIN.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriarthroideae; Oryzaceae; Oryza.
 NC NCB1_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPPONBARE;
 RA Beil C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
 RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsirlin T.,
 RA Riggs F., Hsiao J., Zismann V., Blunt S., Pal G., VanAken S.E.,
 RA Uteback T.R., Feldlyum T.V., Quackenbush J., Salzberg S.L.,
 RA White O., Fraser C.M.;
 RT "Oryza sativa chromosome 3 BAC OSJNB0057P11 genomic sequence."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC084767; AAK72273.1;
 KW Hypothetical protein.
 S0 SEQUENCE 87 AA; 9941 MW; 092E2A6E9D0A42CE CRC64;

Query Match 9.0%; Score 7; DB 10; Length 87;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 LKRRAR 68
 DB 48 LKRRAR 54

RESULT 6
 ID 098268 PRELIMINARY; PRT; 160 AA.
 AC 098268;
 DT 01-OCT-2001 (Tremblrel. 18, Created)
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
 DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
 DE MUR9079 PROTEIN.
 GN MUR9079.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 NC NCB1_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-MAFF30309;
 RA MEDLINE-21082930; PubMed-11214968;
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shlimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL: AP003015; BAB54491.1;
 KW Plasmid; Complete proteome.
 SQ SEQUENCE 160 AA; 17696 MW; 85A9C5A9233D9A50 CRC64;

Query Match
 Best Local Similarity 9.0%; Score 7; DB 16; Length 160;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSITAP 8
 DB 28 TGSITAP 34

RESULT 7
 ID 092XL7 PRELIMINARY; PRT; 160 AA.
 AC 092XL7;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HYPOTHEMETICAL PROTEIN SMA2279.
 GN SMA2279.
 OS Rhizobium melioli (Sinorhizobium melioli).
 OC plasmid pSymb (megaplasmid 1).
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_Taxid-382;
 OX (1)
 RN SEQUENCE FROM N.A.
 RP STRAIN-1021;
 RC MEDLINE-21396509; PubMed-11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barlow-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Curjel M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kallman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yen K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 RT Sinorhizobium melioli pSymb megaplasmid.";
 RT Proc. Natl. Acad. Sci. U.S.A. 98:9883-9886(2001).
 DR EMBL: AE007307; AAK65885.1;
 KW Hypothetical protein; Plasmid; Complete proteome.
 SQ SEQUENCE 160 AA; 17966 MW; 98B4EBE18A1BE34 CRC64;

Query Match
 Best Local Similarity 9.0%; Score 7; DB 16; Length 160;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSITAP 8
 DB 28 TGSITAP 34

RESULT 8
 ID 09JSG7 PRELIMINARY; PRT; 197 AA.
 AC 09JSG7;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE C1142 HYPOTHEMETICAL PROTEIN_2.
 GN CP00259.

OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiales; Chlamydiales.
 OX NCBI_Taxid-83558;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-J138;
 RA MEDLINE-20330349; PubMed-10871362;
 RA Shital M., Hiraoka H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kohara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CML029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 DR EMBL: AP002545; BAA98469.1;
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR InterPro: IPR000531; TonB_box.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
 SQ SEQUENCE 197 AA; 22016 MW; EAA69A27851F790D CRC64;

Query Match
 Best Local Similarity 9.0%; Score 7; DB 16; Length 197;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23
 DB 74 ATGLTSA 80

RESULT 9
 ID 09RBX8 PRELIMINARY; PRT; 228 AA.
 AC 09RBX8;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HYPOTHEMETICAL 24.1 KDA PROTEIN.
 OS Pseudomonas indologera.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Vogesella.
 OX NCBI_Taxid-45465;
 OX (1)
 RN SEQUENCE FROM N.A.
 RP STRAIN-ATCC19706;
 RC van de Loo F.J., Keese P., Llewellyn D.;
 RA "Structural and regulatory genes controlling indigoidine production in
 RT Vogesella indologera: involvement of a peptide synthetase homolog.";
 RL Submitted (SPP-1998) to the EMBL/Genbank/DBJ databases.
 CC -I- SIMILARITY: BELONGS TO THE TETR/ACR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL: AF088856; AAD54003.1;
 DR InterPro: IPR001647; HTH_Tetr.
 DR Pfam: PF00440; tetr.1.
 DR PRINTS: PR00455; HTHTEPR.
 KW DNA-binding; Hypothetical protein; Transcription regulation.
 SQ SEQUENCE 228 AA; 24140 MW; A928DE14F404869B CRC64;

Query Match
 Best Local Similarity 9.0%; Score 7; DB 2; Length 228;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 RRRARP 70
 DB 23 RRRARP 29

RESULT 10
 ID 09T3Y9 PRELIMINARY; PRT; 245 AA.
 AC 09T3Y9;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)

RT EUREUS "1;
 RL Lancer 357:1225-1240(2001).
 DR EMBL: AP003129; BAB41422.1;
 DR EMBL: AP003358; BAB56369.1;
 DR InterPro: IPR000515; BPD_transp.
 DR Pfam: PF00528; BPD_transp. 1.
 KW Complete proteome: Hypothetical protein.
 SO SEQUENCE 387 AA; 43077 MW; 08F9FB4BACADCB8 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 16; Length 387;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 LTSALNTL 26
 |||||
 DB 27 LTSALNTL 33

RESULT 13

O97GC3 PRELIMINARY; PRT; 391 AA.

AC O97GC3;
 DT 01-OCT-2001 (TREMblrel. 18, Created)
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE AICAR TRANSFORMYLASE DOMAIN OF PURH-LIKE PROTEIN.
 GN CAC2445.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 OX NCBI_Taxid=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RA MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dupuis J., Liu D., Hilti J., Wolf Y.I.,
 RA Tatusov R.L., Sabate F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum";
 RT J. Bacteriol. 183:4823-4836(2001).
 DR EMBL: AE007744; AAK80399.1;
 DR InterPro: IPR002695; AICARFT_IPMChas.
 DR Pfam: PF01808; AICARFT_IPMChas. 1.
 DR ProDom: PD004666; AICARFT_IPMChas. 1.
 KW Complete proteome.
 SO SEQUENCE 391 AA; 43547 MW; 18642C6BA97E909E CRC64;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 16; Length 391;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23
 |||||
 DB 58 ATGLTSA 64

RESULT 14

O9AX94 PRELIMINARY; PRT; 392 AA.

AC O9AX94;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE P0501G01.23 PROTEIN.
 GN P0501G01.23.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzae; Oryza.

OX NCBI_Taxid=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0501G01."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP002819; BAB21094.1;
 SO SEQUENCE 392 AA; 40501 MW; BB4F44827A7EDC34 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 10; Length 392;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 RRRARP 70
 |||||
 DB 133 RRRARP 139

RESULT 15

O9PSS8 PRELIMINARY; PRT; 490 AA.

AC O9PSS8;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE PUTATIVE WALL-ASSOCIATED KINASE 2.
 GN H0212B02.2.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzae; Oryza.
 OX NCBI_Taxid=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Han B., Zhou B., Feng Q., Huang Y.C., Chen Z.H., Li Y., Zhu J.J.,
 RA Tang Y.S., Zhao Q., Liu Y.L., Mu J., Yu Z., Fan D.L., Chen L.,
 RA Wang Q.J., Zhang L., Lu Y.Q., Yu S.L., Zhu J., Liu X.H., Hu X.,
 RA Lei H.Y., Zhang Y.J., Wang R., Li C., Lu Y., Chen X.C., Zhang Y.,
 RA Hu H., Jia P.X., Li T., Qian Y.M., Jing K., Hong G.F.;
 RT "Oryza sativa Indica (Guanglu44) genomic DNA, chromosome4, BAC
 RT clone:H0212B02."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL442007; CAC09346.1;
 KW Kinase.
 SO SEQUENCE 490 AA; 52039 MW; 2F1301B08BAZ6EPE CRC64;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 10; Length 490;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 RRRARP 70
 |||||
 DB 345 RRRARP 351

Search completed: June 21, 2002, 08:24:57
 Job time: 282 sec

